



## SEQUENCE LISTING

&lt;110&gt;

Ulrich, Ricky  
Jeddeloh, Jeffrey A.  
Oyston, Petra

&lt;120&gt; Glanders/Melioidosis Vaccines

&lt;130&gt; 003/267/SAP

&lt;140&gt; 10/620,242

&lt;141&gt; 2003-07-15

&lt;150&gt; US 60/386,257

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&lt;160&gt; 44

&lt;170&gt; Apple Macintosh Microsoft Word 6.0

&lt;210&gt; 1

&lt;211&gt; 612

&lt;212&gt; DNA

<213> *B. mallei* ATCC 23344 AHS gene *bmaI1*

&lt;400&gt; 1

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gggttcgagc	gggatcagta	cgatcgcgac	gataccgtct	160
atgtgttcgc	ccgcgacgac	gacggggaaa	tctgcggctg	200
cgcccggctg	ctgccgacga	cccggccgta	tctgctgaag	240
gaactgttcc	cgacgctggt	cgcgcaagac	atgccgttgc	280
cgcaatccgc	cgccgtctgg	gaattgtcgc	gcttcgccgc	320
gaacgccgag	gatccggccg	ggggcgggcaa	cccggcctgg	360
gcggtgcgcc	cgatgctcgc	cgccgtcgtc	gagtgcgccg	400
cgcggtttgg	cgcgaaagcaa	ctgatcgggc	tgacgtttct	440
gagcatggag	cgcctgttcc	gccggatcgg	cgtgcacgcg	480
caccggggcg	ggcccgcgca	gcagatcgac	gggcgcattg	520
tcgtcgcgtg	ctggatcgac	ctcgacgcgc	aaacgctcgc	560
cgcgctcgat	ctcgaccgcg	tgctgtgcgc	gccgcccgcg	600
gaagccgcct	ga			612

&lt;210&gt; 2

&lt;211&gt; 609

&lt;212&gt; DNA

<213> *B. mallei* ATCC 23344 AHS gene *bmaI3*

&lt;400&gt; 2

atgtcataca	tcattcgcg	ccgattgaac	gaactgccgc	40
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cgcacgtcca gaccgatctc ggcgcgtatc gctacgacgt 80
gttcgtgcgc cggctcggct ggacgatcgc cggccactcg 120
ctcgacgaac atgcggagtg ggacgagttc gacgggccgt 160
cgacgattca tgtcgtcgcg ctcgacgacg cgcgcgagat 200
ctgcggctac gcacgcctgc tgccgacgac gggcccgtat 240
ctgctgcgcg acgtgtttgc gcatctgctc ggctcgtcgc 280
ccgcgcgcga atcgccctgc gtctgggaaa tgtcgcgctt 320
cgccgcgctc cggcggcggc gaagcgcgac cgagcgcgag 360
ccgctcggca tggcgcttct tccgtcggtg ctcacgggtg 400
ccgcgtcgct cggcgcgacg cgcgtggtcg gcgtgatgac 440
gccatcgatc gaacgcctgt accgccgctc gggcatcgcg 480
ctgcatcgcc tcggcaacgc gatgccgggc gcgggcggca 520
gcctgtccgc atgctcgatc gatctgccgc gcctcgcgtt 560
cgcgccggtg ggcctcaagc agtgccgggc gtgcctggcg 600
atgcattga 609

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<210> 3

<211> 720

<212> DNA

<213> *B. mallei* ATCC 23344 transcriptional regulator gene  
*bmaR1*

<400> 3

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ccgcggagaa cgagcagcag ctcttccaac agatcgccgc 80
gtatacgaag cggctcggct tcgaatattg ctgctatggc 120
atacgcgtgc cgttgccgat ctogaagccg gtcgtcgcga 160
ttttcgacac ctatccgaac ggctggatgg agcgctacca 200
ggaaatgaac tacctggagg tcgatccgac cgtacgcgag 240
ggcgcgctca gctcgaacat gatcgtcttg ccggaggcga 280
gcgcgagcga cgcgacgacg ctctggagcg acgcgcgcga 320
tcacgggctg gcggtcggcg tcgcgcagtc gagctggggc 360
tcgcgcgggg tgttcggtct cctgacgata gcgcggcaca 400
cggaccgcct gacgtccgcc gagatcaacc atctgacgtt 440
gcaggcgaac tggctcgcga acatgtcgca ctcgctgatg 480
agccgttttc tcgtgccgaa gctcgcgccc gaatcggggc 520
tggcgctcac gcaccgcgag cgggaggtgc tgtgctggac 560
gggagagggc aagaccgcgt gcgagatcgg gcagatcctc 600
agcatctccg agcgcacggt gaactttcac gtcaacaaca 640
tcctcgacaa gctcggcgcg acgaacaagg tgcaggccgt 680
cgtgaaggcg atcgcgatgg ggctcatcga cgcgccgtaa 720

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<210> 4

<211> 609

<212> DNA

<213> *B. mallei* ATCC 23344 transcriptional regulator gene  
*bmaR3*

<400> 4

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cgcacgtcca gaccgatctc ggcgcgtatc gctacgacgt 80
gttcgtgcgc cggctcggct ggacgatcgc cggccactcg 120
ctcgacgaac atgcggagtg ggacgagttc gacgggccgt 160
cgacgattca tgtcgtcgcg ctcgacgacg cgcgcgagat 200
ctgcggctac gcacgcctgc tgccgacgac gggcccgtat 240

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ctgctgcgcg acgtgtttgc gcatctgctc ggctcgtcgc 280
ccgcgcgcga atcgccctgcc gtctgggaaa tgtcgcgctt 320
cgccgcgtcg cggcggcggc gaagcgcgac cgaccgcgag 360
ccgctcggca tggcgttctt tccgtcgggtg ctcacgggtgg 400
ccgcgtcgct cggcgcgacg cgcgtgggtcg gcgtgatgac 440
gccatcgatc gaacgcctgt accgccgctc gggcatcgcg 480
ctgcatcgcc tcggcaacgc gatgccgggc gcgggcggca 520
gcctgtccgc atgctcgatc gatctgccgc gcctcgcgtt 560
cgcgccggtt ggcctcaagc agtgcgcggc gtgcctggcg 600
atgcattga 609

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<210> 5

<211> 660

<212> DNA

<213> *B. mallei* ATCC 23344 transcriptional regulator gene  
*bmaR4*

<400> 5

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agcagcgcgg tgcgccgctg gcggcccgtc gcccgtcgag 80
aacgctacgt tcggcgacga gaccgggggc gccgcgtgcg 120
cggacgggtct tgcgggcatg tcctgttcga tcgtcggccg 160
acgcttgctg cgtgcgtgtc gagtccgcgc acaatcaccc 200
gcagcgggtct tcagcgggtct ttccggcgcg gacgcctggc 240
ccgccatgcg tacgagggcg catggcgcgag catgttcgcg 280
gcctgcgggg gcggcgctga gcgtgcgcgg cggcagccgt 320
gatgcagggt tggccggcg gcgcgggatt cgagcgatgc 360
tcgagcgcgc agcgcgggtt cggcttcggc gcaggcggcc 400
gattgtcccc ccgcgttcga cgaaacgaac ggcgtgccgt 440
gcttcggcgg cgccgcaggc aagctcgccg gcgtttcgcc 480
gcgcgcgggc cgccgttgcc ctctcgcccc ttctgagcac 520
gctttcttca ttggttcgct aacgtaactt cctcacttga 560
gctgggcggg tctatgttcg aaggcttgtc cattgggtcg 600
tttaacgaaa ttctgaacgc gacttgcaag aagagcctct 640
ttgagcagac ggcgtatcac 660

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<210> 6

<211> 726

<212> DNA

<213> *B. mallei* ATCC 23344 transcriptional regulator gene  
*bmaR5*

<400> 6

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cggggctcga cagcgcacga tccgaggaag aggcgtttcg 80
aagcgtcgaa accgcggcgg cggcgctcga ttctgaatac 120
tgcgcatacg ggctgcgcgt gccgtggccg ctgtccaggc 160
cgcgcatcga gacgcgcagc aactttcccg agcaatggaa 200
gcggcgctac gtcgaggcgg gtttcctcga tgtcgatccg 240
attctcgcgc acggccgcgc atcgagcaa ccggtcgtcc 280
tcgccgagac gctgttttgc tccgcgcacc agatgtgggt 320
cgaggcgcag tcgttcgggt tgcggttcgg ctgggcgcag 360
tcgagcttcg acgcgtatgg cggcatgggc atgctcgcgc 400
tcgtccgctc gcgcgagccg gtgacggcgg cggaactcga 440
cgcgaaggag taccggatgc gctggctcgt gcgcaccgcg 480
cacgccgcgc tcggccgcac gatgttgccc aagctgatgg 520

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cggacccgga ggcggggctg accgagcgcg aggtcgaggt 560
gctcaagtgg ggcggcgacg gcaagacgtc cggcgagatc 600
tcgaagatcc tcgcatatc cgtcgatacg gtgaatttcc 640
acgtgaagaa cgcgatcctg aagctcagga cggcgaacaa 680
gacggcggcc gtcgtgcgcg cggcgatgct cgggttgctg 720
agctga 726

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<210> 7

<211> 612

<212> DNA

<213> *B. pseudomallei* DD503 AHS gene *bpmI1*

<400> 7

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atgcgaactt tcgttcatgg cgacggggcg ctgccgagcg 40
acttggcggc tgatctgggc ctttatcggc acggagtttt 80
cgtcgagcag ctcggctgga aactgccgtc ggcaagcgaa 120
gggttcgagc gggatcagta cgatcgcgac gataccgtct 160
atgtgttcgc ccgcgacgac gacggggaaa tctgcggctg 200
cgcccggctg ctgccgacga cccggccgta tctgctgaag 240
gaactgttcc cgacgtgtgt cgcgcaagac atgccgttgc 280
cgcaatccgc cgccgtcttg gaattgtcgc gtttcgccgc 320
gaacgccgag gatccggccg ggggcggcaa cccggccttg 360
gcggtgcggc cgatgctcgc cgccgtcgtc gagtgcgccg 400
cgcggtcttg cgcgaaagcaa ctgatcggcg tgacgtttct 440
gagcatggag cgctgtttcc gccggatcgg cgtgcacgcg 480
caccgggcgg ggcccgcgca gcagatcgac gggcgcatgg 520
tcgtcgcggt ctggatcgac ctcgacgcgc aaacgctcgc 560
cgcgctcgat ctcgaccgcg tgctgtgcgc gccgcccgcg 600
gaagccgcct ga 612

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<210> 8

<211> 621

<212> DNA

<213> *B. pseudomallei* DD503 AHS gene *bpmI2*

<400> 8

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ccaccgtcaa ggcagcactc ggcaattatc gtcgggcat 80
attcatcgag aaactcggct ggccattgcc gttggtcgac 120
gggctcgaga tcgatcagtt cgatcgtccc gatacgattt 160
acgtggtcgg caaaacagag tccggcgata tctgcggatg 200
cgcccgcctg ctgccacgca cgaggcccta cctgctcgga 240
gaggtgttcc ccatctgat gggcgacgcg gcgccgcct 280
gctcggcgca cgtgtgggaa atctcgcgat tttcgtcttc 320
gatcctctcc ggagggccgg acgcgctgcg gcaggctcac 360
cgcaatacgc gcacctctgt cgcgaaaatc gtccgctttg 400
cgcaggcggc cggcgtgaag cggctgatca ccgtttcgcc 440
gctcgcagtc gagcggctgc tcaaccgtct gaaagtccat 480
attcacgcg cggttcgcgc tcggttgatc gacggcaagc 520
cggtgttcgc gtgctggatc gaggtggacg acatcacgct 560
ccaagcgctc gacatcgagc cggccgcgca ttcggccgcc 600
ggcgcgctgc gccattcgtg a 621

```

<210> 9

<211> 609

<212> DNA

<213> *B. pseudomallei* DD503 AHS gene *bpmI3*

<400> 9

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cgcacgtcca	gaccgatctc	ggcgcgtatc	gctacgacgt	80
gttcgtgcgc	cggctcggct	ggacgatcgc	cggccactcg	120
ctcgacgaac	atgcggagt	ggacgagttc	gacggggccgt	160
cgacgattca	tgtcgtcgcg	ctcgacgacg	cgcgcgagat	200
ctgcggctac	gcacgcctgc	tgccgacgac	gggcccgtat	240
ctgctgcgcg	acgtgtttgc	gcattctgctc	ggctcgtcgc	280
ccgcgcgcga	atcgccctgcc	gtctgggaaa	tgtcgcgctt	320
cgcgcgcgtc	cggcggcggc	gaagcgcgac	cgagcgcgag	360
ccgctcggca	tggcgcttctt	tccgtcgggtg	ctcacgggtgg	400
ccgcgtcgc	cggcgcgacg	cgcgtgggtc	gcgtgatgac	440
gccatcgatc	gaacgcctgt	accgccgctc	gggcatcgcg	480
ctgcatcgcc	tcggcaacgc	gatgccgggc	gcgggcggca	520
gcctgtccgc	atgctcgatc	gatctgccgc	gcctcgcggt	560
cgcgcgcgtt	ggccgcaagc	agtgcgcggc	gtgcctggcg	600
atgcattga				609

<210> 10

<211> 720

<212> DNA

<213> *B. pseudomallei* DD503 transcription regulator gene  
*bpmR1*

<400> 10

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gtatacgaag	cggctcggct	tccaatattg	ctgctatggc	120
atacgcgtgc	cgttgccgat	ctcgaagccg	gtcgtcgcga	160
ttttcgacac	ctatccgaac	ggctggatgg	agcgtacca	200
ggaaatgaac	tacctggagg	tcgatccgac	cgtacgcgag	240
ggcgcgctca	gctcgaacat	gatcgtcttg	ccggaggcga	280
gcgcgagcga	cgcgacgacg	ctctggagcg	acgcgcgcga	320
tcacgggctg	gcggtcggcg	tcgcgcagtc	gagctggggc	360
tcgcgcgggg	tgttcggtct	cctgacgatc	gcgcggcaca	400
ccgaccgcct	gacgtccgcc	gagatcaacc	atctgacggt	440
gcaggcgaac	tggctcgcga	acatgtcgca	ctcgtctgatg	480
agccgttttc	tcgtgccgaa	gctcgcgcgc	gaatcggggc	520
tggcgtcac	gcaccgcgag	cgggaggtgc	tgtgctggac	560
gggggagggc	aagaccgcgt	gcgagatcgg	gcagatcctc	600
agcatctccg	agcgcacggt	gaactttcac	gtcaacaaca	640
tcctcgacaa	gctcggcgcg	acgaacaagg	tgcaggccgt	680
cgtgaaggcg	atcgcgatgg	ggctcatcga	cgcgccgtaa	720

<210> 11

<211> 711

<212> DNA

<213> *B. pseudomallei* DD503 transcription regulator gene  
*bpmR2*

<400> 11

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tacggcatgc	gccgcccctt	tccgatcagc	aatccgccga	160

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tcctcatggt gtccaactat cccgcccgat ggcaggaacg 200
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aaggccgcgc tcggcagcga cccgcccgtg acctggagcg 280
cgcccgccaa cgcacgaaa agcgcattct gggcgaggcg 320
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agcatctcgg agagcaccgt caattttcac gtgaagaata 640
tcgtctccaa gctgggctcc acgaacaaga tacaggccgt 680
ggccaaggcc gcgctgatgg ggatgctgtg a 711

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<210> 12

<211> 693

<212> DNA

<213> *B. pseudomallei* DD503 transcription regulator gene  
*bpmR3*

<400> 12

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ccgttctcgt ggaacgacgt cgcgacggcg aacctgcgcg 280
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caacggcatc agcatcccg tgcatcagcc gctcggacgc 360
gtgctgctgg tgagcctgtc cggcaccgcg ccgacgcacg 400
atgccgatgc gaaatggcgc aacgcgtacc tgctcggcat 440
gcagttcaat ctgcagttcc agagcatgcg cacgtgccgc 480
ccgattccgc cgtccgtcca cctgacggat cgcgaacaga 520
tgtgcctcac gtgggtcgcg cgcggcaagt cgtcgtgggt 560
catcgcgaa atgctcgaca tctccaaata cacggtcgac 600
ttccacatcg agaacgcgat ggagaagctc aacacgcgca 640
gccgcacgtt cgccgccgtg aaggcgacgc ggcaggggct 680
catctttcca tga 693

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<210> 13

<211> 885

<212> DNA

<213> *B. pseudomallei* DD503 transcription regulator gene  
*bpmR4*

<400> 13

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cgcccgccgc acaggcgggt cgcgcgcgcg tcgcgcgcaa 120
ccgcttgccg gcggcgggcg cgcgcgctca gatcaaccgc 160
cgcgccgatg cgatgacgac cgctgcgcg cggttgttcg 200
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gccgtcttgc cgcgccccgc cactgcagc gattcgcgct 320

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cgcgcgcggt cagatcgcac gagccctgcc gtctgagccg 360
gcaatcgagc agctcgtgca tcgccgctg cacgaagctc 400
gcgagcaact gcgacaggct cagcagccgc agtatgtcgc 440
tcgctcgtg ctcgaacgga tcgtcggtcg ccatgctgag 480
catgctgac ggcgcgtgc gatcgtgaac ggggcaactg 520
agcccgtaga cgaggccgta cgatttcgcc tcgtcgcgca 560
tgagcttcgc gcggtcggtc gtatagaggt cgtcgtgcca 600
gatgagcggc acggtcgggc accggcaatg ctgaacgacg 640
ggatcgatcg acaggtagtc ggcggcgtcg tagcgcagcc 680
gccactcggc cggaatccg tcgagcatgc agcggctcga 720
cgccgcgccg gagatctgat gccggtacgc gaaattcttg 760
aaccccagtt ggcgaacgtg atacgccgtc tgctcaaaga 800
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accaatggac aagccttcga acatagaacc gcccagctca 880
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<210> 14

<211> 726

<212> DNA

<213> *B. pseudomallei* DD503 transcription regulator gene  
*bpmR5*

<400> 14

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tgcgcatacg ggctgcgcgt gccgtggccg ctgtccaggc 160
cgcgcatcga gacgcgcagc aactttcccg agcaatggaa 200
gcggcgctac gtcgaggcgg gtttcctcga cgtcgatccg 240
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tcgccgagac gctgttttgcg tccgcgcacc agatgtgggt 320
cgaggcgcag tcgttcgggt tgcggttcgg ctgggcgcag 360
tcgagcttcg acgcgtatgg cggcatgggc atgctcgcgc 400
tcgtccgctc gtgcgagccg gtgacggcgg cggaaactcga 440
cgcgaaaggag taccggatgc gctggctcgt gcgcaccgcg 480
cacgccgcgc tcggccgcac gatgttgccc aagctgatgg 520
cggacccgga gcgcgggctg accgagcgcg aggtcgaggt 560
gctcaagtgg gcggcggacg gcaagacgtc cggcgagatc 600
tcgaagatcc tcgcgatatc cgtcgatacg gtgaatttcc 640
acgtgaagaa cgcgatcctg aagctcagga cggcgaacaa 680
gacggcggcc gtcgtgcgcg cggcgatgct cgggttgctg 720
agctga 726

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<210> 15

<211> 203

<212> PRT

<213> *B. mallei* ATCC 23344 bmaI1

<400> 15

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Leu Tyr Arg His Gly Val Phe Val Glu Gln
             25             30

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Leu	Gly	Trp	Lys	Leu	Pro	Ser	Ala	Ser	Glu	
				35					40	
Gly	Phe	Glu	Arg	Asp	Gln	Tyr	Asp	Arg	Asp	
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Asp	Thr	Val	Tyr	Val	Phe	Ala	Arg	Asp	Asp	
				55					60	
Gly	Glu	Ile	Cys	Gly	Cys	Ala	Arg	Leu	Leu	
				65					70	
Pro	Thr	Thr	Arg	Pro	Tyr	Leu	Leu	Lys	Glu	
				75					80	
Lys	Phe	Pro	Thr	Leu	Val	Ala	Gln	Asp	Met	
				85					90	
Pro	Leu	Pro	Gln	Ser	Ala	Ala	Val	Trp	Glu	
				95					100	
Leu	Ser	Arg	Phe	Ala	Ala	Asn	Ala	Glu	Asp	
				105					110	
Pro	Ala	Gly	Gly	Gly	Asn	Pro	Ala	Trp	Ala	
				115					120	
Val	Arg	Pro	Met	Leu	Ala	Ala	Val	Val	Glu	
				125					130	
Cys	Ala	Ala	Arg	Leu	Gly	Ala	Lys	Gln	Leu	
				135					140	
Ile	Gly	Val	Thr	Phe	Leu	Ser	Met	Glu	Arg	
				145					150	
Leu	Phe	Arg	Arg	Ile	Gly	Val	His	Ala	His	
				155					160	
Arg	Ala	Gly	Pro	Ala	Gln	Gln	Ile	Asp	Gly	
				165					170	
Arg	Met	Val	Val	Ala	Cys	Trp	Ile	Asp	Leu	
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Asp	Ala	Gln	Thr	Leu	Ala	Ala	Leu	Asp	Leu	
				185					190	
Asp	Leu	Pro	Leu	Leu	Cys	Ala	Pro	Pro	Ala	
				195					200	
Glu	Ala	Ala								

&lt;210&gt; 16

&lt;211&gt; 202

&lt;212&gt; PRT

<213> *B. mallei* ATCC 23344 bmaI3

&lt;400&gt; 16

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				15					20	
Gly	Ala	Tyr	Arg	Tyr	Asp	Val	Phe	Val	Arg	
				25					30	
Arg	Leu	Gly	Trp	Thr	Ile	Ala	Gly	His	Ser	
				35					40	
Leu	Asp	Glu	His	Ala	Glu	Trp	Asp	Glu	Phe	
				45					50	
Asp	Gly	Pro	Ser	Thr	Ile	His	Val	Val	Ala	
				55					60	



Leu	Asp	Asp	Ala	Arg	Glu	Ile	Cys	Gly	Tyr	
				65					70	
Ala	Arg	Leu	Leu	Pro	Thr	Thr	Gly	Pro	Tyr	
				75					80	
Leu	Leu	Arg	Asp	Val	Phe	Ala	His	Leu	Leu	
				85					90	
Gly	Ser	Ser	Pro	Ala	Pro	Gln	Ser	Pro	Ala	
				95					100	
Val	Trp	Glu	Met	Ser	Arg	Phe	Ala	Ala	Ser	
				105					110	
Arg	Arg	Arg	Arg	Ser	Ala	Thr	Glu	Arg	Glu	
				115					120	
Pro	Leu	Gly	Met	Ala	Phe	Phe	Pro	Ser	Val	
				125					130	
Leu	Thr	Val	Ala	Ala	Ser	Leu	Gly	Ala	Thr	
				135					140	
Arg	Val	Val	Gly	Val	Met	Thr	Pro	Ser	Ile	
				145					150	
Glu	Arg	Leu	Tyr	Arg	Arg	Ser	Gly	Ile	Ala	
				155					160	
Leu	His	Arg	Leu	Gly	Asn	Ala	Met	Pro	Gly	
				165					170	
Ala	Gly	Gly	Ser	Leu	Ser	Ala	Cys	Ser	Ile	
				175					180	
Asp	Leu	Pro	Arg	Leu	Ala	Phe	Ala	Pro	Leu	
				185					190	
Gly	Leu	Lys	Gln	Cys	Ala	Ala	Cys	Leu	Ala	
				195					200	

Met His

&lt;210&gt; 17

&lt;211&gt; 239

&lt;212&gt; PRT

<213> *B. mallei* ATCC 23344 bmaR1

&lt;400&gt; 17

Met	Glu	Leu	Arg	Trp	Gln	Asp	Ala	Tyr	Leu	
1				5					10	
Gln	Phe	Ser	Ala	Ala	Glu	Asn	Glu	Gln	Gln	
				15					20	
Leu	Phe	Gln	Gln	Ile	Ala	Ala	Tyr	Thr	Lys	
				25					30	
Arg	Leu	Gly	Phe	Glu	Tyr	Cys	Cys	Tyr	Gly	
				35					40	
Ile	Arg	Val	Pro	Leu	Pro	Ile	Ser	Lys	Pro	
				45					50	
Val	Val	Ala	Ile	Phe	Asp	Thr	Tyr	Pro	Asn	
				55					60	
Gly	Trp	Met	Glu	Arg	Tyr	Gln	Glu	Met	Asn	
				65					70	
Tyr	Leu	Glu	Val	Asp	Pro	Thr	Val	Arg	Glu	
				75					80	
Gly	Ala	Leu	Ser	Ser	Asn	Met	Ile	Val	Trp	
				85					90	

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Pro Glu Ala Ser Ala Ser Asp Ala Thr Thr
      95                      100
Leu Trp Ser Asp Ala Arg Asp His Gly Leu
      105                      110
Ala Val Gly Val Ala Gln Ser Ser Trp Ala
      115                      120
Ser Arg Gly Val Phe Gly Leu Leu Thr Ile
      125                      130
Ala Arg His Thr Asp Arg Leu Thr Ser Ala
      135                      140
Glu Ile Asn His Leu Thr Leu Gln Ala Asn
      145                      150
Trp Leu Ala Asn Met Ser His Ser Leu Met
      155                      160
Ser Arg Phe Leu Val Pro Lys Leu Ala Pro
      165                      170
Glu Ser Gly Val Ala Leu Thr His Arg Glu
      175                      180
Arg Glu Val Leu Cys Trp Thr Gly Glu Gly
      185                      190
Lys Thr Ala Cys Glu Ile Gly Gln Ile Leu
      195                      200
Ser Ile Ser Glu Arg Thr Val Asn Phe His
      205                      210
Val Asn Asn Ile Leu Asp Lys Leu Gly Ala
      215                      220
Thr Asn Lys Val Gln Ala Val Val Lys Ala
      225                      230
Ile Ala Met Gly Leu Ile Asp Ala Pro
      235

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<210> 18

<211> 202

<212> PRT

<213> *B. mallei* ATCC 23344 bmaR3

<400> 18

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Met Ser Tyr Ile Ile Ala Gly Arg Leu Asn
  1           5                      10
Glu Leu Pro Pro His Val Gln Thr Asp Leu
           15                      20
Gly Ala Tyr Arg Tyr Asp Val Phe Val Arg
           25                      30
Arg Leu Gly Trp Thr Ile Ala Gly His Ser
           35                      40
Leu Asp Glu His Ala Glu Trp Asp Glu Phe
           45                      50
Asp Gly Pro Ser Thr Ile His Val Val Ala
           55                      60
Leu Asp Asp Ala Arg Glu Ile Cys Gly Tyr
           65                      70
Ala Arg Leu Leu Pro Thr Thr Gly Pro Tyr
           75                      80
Leu Leu Arg Asp Val Phe Ala His Leu Leu
           85                      90

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Gly	Ser	Ser	Pro	Ala	Pro	Gln	Ser	Pro	Ala	
				95						100
Val	Trp	Glu	Met	Ser	Arg	Phe	Ala	Ala	Ser	
				105						110
Arg	Arg	Arg	Arg	Ser	Ala	Thr	Glu	Arg	Glu	
				115						120
Pro	Leu	Gly	Met	Ala	Phe	Phe	Pro	Ser	Val	
				125						130
Leu	Thr	Val	Ala	Ala	Ser	Leu	Gly	Ala	Thr	
				135						140
Arg	Val	Val	Gly	Val	Met	Thr	Pro	Ser	Ile	
				145						150
Glu	Arg	Leu	Tyr	Arg	Arg	Ser	Gly	Ile	Ala	
				155						160
Leu	His	Arg	Leu	Gly	Asn	Ala	Met	Pro	Gly	
				165						170
Ala	Gly	Gly	Ser	Leu	Ser	Ala	Cys	Ser	Ile	
				175						180
Asp	Leu	Pro	Arg	Leu	Ala	Phe	Ala	Pro	Leu	
				185						190
Gly	Leu	Lys	Gln	Cys	Ala	Ala	Cys	Leu	Ala	
				195						200

Met His

<210> 19  
 <211> 220  
 <212> PRT  
 <213> *B. mallei* ATCC 23344 bmaR4  
 <400> 19

Met	Pro	Leu	Pro	Ile	Arg	Cys	Gly	Glu	Gly	
1				5						10
Pro	Ser	Pro	Gln	Gln	Arg	Gly	Ala	Pro	Arg	
				15						20
Ala	Ala	Arg	Arg	Pro	Ser	Arg	Thr	Leu	Arg	
				25						30
Ser	Ala	Thr	Arg	Pro	Gly	Ala	Pro	Arg	Ala	
				35						40
Arg	Thr	Val	Leu	Arg	Ala	Cys	Pro	Val	Arg	
				45						50
Ser	Ser	Ala	Asp	Ala	Cys	Val	Val	Arg	Val	
				55						60
Glu	Ser	Ala	Asp	Asn	His	Pro	Gln	Arg	Ser	
				65						70
Ser	Ala	Val	Phe	Arg	Arg	Ala	Thr	Pro	Gly	
				75						80
Pro	Pro	Cys	Val	Arg	Gly	Arg	Met	Ala	Gln	
				85						90
His	Val	Arg	Gly	Leu	Pro	Gly	Arg	Arg	Arg	
				95						100
Ala	Cys	Ala	Ala	Ala	Ala	Val	Met	Gln	Val	
				105						110
Trp	Pro	Ala	Arg	Ala	Gly	Phe	Glu	Arg	Cys	
				115						120

Ser	Ser	Ala	Glu	Arg	Arg	Phe	Gly	Phe	Gly
				125					130
Ala	Gly	Gly	Arg	Leu	Ser	Arg	Arg	Val	Arg
				135					140
Arg	Asn	Glu	Arg	Arg	Ala	Val	Leu	Arg	Arg
				145					150
Arg	Gly	Arg	Gln	Ala	Arg	Arg	Arg	Phe	Ala
				155					160
Ala	Arg	Gly	Pro	Pro	Leu	Pro	Ser	Arg	Pro
				165					170
Phe	Arg	Ala	Arg	Phe	Leu	His	Trp	Phe	Ala
				175					180
Asn	Val	Thr	Ser	Ser	Leu	Glu	Leu	Gly	Gly
				185					190
Ser	Met	Phe	Glu	Gly	Leu	Ser	Ile	Gly	Ser
				195					200
Phe	Asn	Glu	Ile	Leu	Asn	Ala	Thr	Cys	Lys
				205					210
Lys	Ser	Leu	Phe	Glu	Gln	Thr	Ala	Tyr	His
				215					220

&lt;210&gt; 20

&lt;211&gt; 241

&lt;212&gt; PRT

<213> *B. mallei* ATCC 23344 bmar5

&lt;400&gt; 20

Met	Arg	Ala	Ala	Met	Gly	Asn	Trp	Ala	Glu
1				5					10
Asp	Leu	Leu	Ala	Gly	Leu	Asp	Ser	Ala	Arg
				15					20
Ser	Glu	Glu	Glu	Arg	Phe	Arg	Ser	Val	Glu
				25					30
Thr	Ala	Ala	Ala	Ala	Leu	Asp	Phe	Glu	Tyr
				35					40
Cys	Ala	Tyr	Gly	Leu	Arg	Val	Pro	Trp	Pro
				45					50
Leu	Ser	Arg	Pro	Arg	Ile	Glu	Thr	Arg	Ser
				55					60
Asn	Phe	Pro	Glu	Gln	Trp	Lys	Arg	Arg	Tyr
				65					70
Val	Glu	Ala	Gly	Phe	Leu	Asp	Val	Asp	Pro
				75					80
Ile	Leu	Ala	His	Gly	Arg	Arg	Ser	Gln	Gln
				85					90
Pro	Val	Val	Leu	Ala	Glu	Thr	Leu	Phe	Ala
				95					100
Ser	Ala	His	Gln	Met	Trp	Val	Glu	Ala	Gln
				105					110
Ser	Phe	Gly	Leu	Arg	Phe	Gly	Trp	Ala	Gln
				115					120
Ser	Ser	Phe	Asp	Ala	Tyr	Gly	Gly	Met	Gly
				125					130
Met	Leu	Ala	Leu	Val	Arg	Ser	Arg	Glu	Pro

				135					140
Val	Thr	Ala	Ala	Glu	Leu	Asp	Ala	Lys	Glu
				145					150
Tyr	Arg	Met	Arg	Trp	Leu	Val	Arg	Thr	Ala
				155					160
His	Ala	Ala	Leu	Gly	Arg	Met	Met	Leu	Pro
				165					170
Lys	Leu	Met	Ala	Asp	Pro	Glu	Arg	Glu	Leu
				175					180
Thr	Glu	Arg	Glu	Val	Glu	Val	Leu	Lys	Trp
				185					190
Ala	Ala	Asp	Gly	Lys	Thr	Ser	Gly	Glu	Ile
				195					200
Ser	Lys	Ile	Leu	Ala	Ile	Ser	Val	Asp	Thr
				205					210
Val	Asn	Phe	His	Val	Lys	Asn	Ala	Ile	Leu
				215					220
Lys	Leu	Arg	Thr	Ala	Asn	Lys	Thr	Ala	Ala
				225					230
Val	Val	Arg	Ala	Ala	Met	Leu	Gly	Leu	Leu
				235					240
Ser									

<210> 21  
 <211> 203  
 <212> PRT  
 <213> *B. pseudomallei* DD503 bpmI1  
 <400> 21

Met	Arg	Thr	Phe	Val	His	Gly	Asp	Gly	Arg
1				5					10
Leu	Pro	Ser	Asp	Leu	Ala	Ala	Asp	Leu	Gly
				15					20
Leu	Tyr	Arg	His	Gly	Val	Phe	Val	Glu	Gln
				25					30
Leu	Gly	Trp	Lys	Leu	Pro	Ser	Ala	Ser	Glu
				35					40
Gly	Phe	Glu	Arg	Asp	Gln	Tyr	Asp	Arg	Asp
				45					50
Asp	Thr	Val	Tyr	Val	Phe	Ala	Arg	Asp	Asp
				55					60
Asp	Gly	Glu	Ile	Cys	Gly	Cys	Ala	Arg	Leu
				65					70
Lue	Pro	Thr	Thr	Arg	Pro	Tyr	Leu	Leu	Lys
				75					80
Glu	Leu	Glu	Pro	Thr	Leu	Val	Ala	Gln	Asp
				85					90
Met	Pro	Leu	Pro	Gln	Ser	Ala	Ala	Val	Trp
				95					100
Glu	Leu	Ser	Arg	Phe	Ala	Ala	Asn	Ala	Glu
				105					110
Asp	Pro	Ala	Gly	Gly	Gly	Asn	Pro	Ala	Trp
				115					120
Ala	Val	Arg	Pro	Met	Leu	Ala	Ala	Val	Val

	125		130
Glu Cys Ala Ala Arg	Leu Gly Ala Lys Gln		
	135		140
Leu Ile Gly Val Thr	Phe Leu Ser Met Glu		
	145		150
Arg Leu Phe Arg Arg	Ile Gly Val His Ala		
	155		160
His Arg Ala Gly Pro	Ala Gln Gln Ile Asp		
	165		170
Gly Arg Met Val Val	Ala Cys Trp Ile Asp		
	175		180
Leu Asp Ala Gln Thr	Leu Ala Ala Leu Asp		
	185		190
Leu Asp Pro Leu Leu	Cys Ala Pro Pro Ala		
	195		200
Glu Ala Ala			

<210> 22  
 <211> 206  
 <212> PRT  
 <213> *B. pseudomallei* DD503 bpmI2  
 <400> 22

Met Ile Asp Thr Thr	Val Ile Ser Ala Ala		
1	5		10
Gln Leu Asp Ser Thr	Val Lys Ala Ala Leu		
	15		20
Gly Asn Tyr Arg Arg	Ala Ile Phe Ile Glu		
	25		30
Lys Leu Gly Trp Pro	Leu Pro Leu Val Asp		
	35		40
Gly Leu Glu Ile Asp	Gln Phe Asp Arg Pro		
	45		50
Asp Thr Ile Tyr Val	Val Gly Lys Thr Glu		
	55		60
Ser Gly Asp Ile Cys	Gly Cys Ala Arg Leu		
	65		70
Leu Pro Thr Thr Arg	Pro Tyr Leu Leu Gly		
	75		80
Glu Val Phe Pro Asp	Leu Met Gly Asp Ala		
	85		90
Ala Pro Pro Cys Ser	Ala His Val Trp Glu		
	95		100
Ile Ser Arg Phe Ser	Ser Ser Ile Leu Ser		
	105		110
Gly Gly Pro Asp Ala	Leu Arg Gln Ala His		
	115		120
Arg Asn Thr Arg Ile	Leu Leu Ala Lys Ile		
	125		130
Val Arg Phe Ala Gln	Ala Ala Gly Val Lys		
	135		140
Arg Leu Ile Thr Val	Ser Pro Leu Ala Val		
	145		150
Glu Arg Leu Leu Asn	Arg Leu Lys Val His		

				155					160
Ile	His	Arg	Ala	Gly	Pro	Pro	Arg	Leu	Ile
				165					170
Asp	Gly	Lys	Pro	Val	Phe	Ala	Cys	Gln	Ile
				175					180
Glu	Val	Asp	Asp	Ile	Thr	Leu	Gln	Ala	Leu
				185					190
Asp	Ile	Glu	Pro	Ala	Ala	Asp	Ser	Ala	Ala
				195					200
Gly	Ala	Leu	Arg	His	Ser				
				205					

&lt;210&gt; 23

&lt;211&gt; 202

&lt;212&gt; PRT

<213> *B. pseudomallei* DD503 bpmI3

&lt;400&gt; 23

Met	Ser	Tyr	Ile	Ile	Ala	Gly	Arg	Leu	Asn
1				5					10
Glu	Leu	Pro	Pro	His	Val	Gln	Thr	Asp	Leu
				15					20
Gly	Ala	Tyr	Arg	Tyr	Asp	Val	Phe	Val	Arg
				25					30
Arg	Leu	Gly	Trp	Thr	Ile	Ala	Gly	His	Ser
				35					40
Leu	Asp	Glu	His	Ala	Glu	Trp	Asp	Glu	Phe
				45					50
Asp	Gly	Pro	Ser	Thr	Ile	His	Val	Val	Ala
				55					60
Leu	Asp	Asp	Ala	Arg	Glu	Ile	Cys	Gly	Tyr
				65					70
Ala	Arg	Leu	Leu	Pro	Thr	Thr	Gly	Pro	Tyr
				75					80
Leu	Leu	Arg	Asp	Val	Phe	Ala	His	Leu	Leu
				85					90
Gly	Ser	Ser	Pro	Ala	Pro	Gln	Ser	Pro	Ala
				95					100
Val	Trp	Glu	Met	Ser	Arg	Phe	Ala	Ala	Ser
				105					110
Arg	Arg	Arg	Arg	Ser	Ala	Thr	Glu	Arg	Glu
				115					120
Pro	Leu	Gly	Met	Ala	Phe	Phe	Pro	Ser	Val
				125					130
Leu	Thr	Val	Ala	Ala	Ser	Leu	Gly	Ala	Thr
				135					140
Arg	Val	Val	Gly	Val	Met	Thr	Pro	Ser	Ile
				145					150
Glu	Arg	Leu	Tyr	Arg	Arg	Ser	Gly	Ile	Ala
				155					160
Leu	His	Arg	Leu	Gly	Asn	Ala	Met	Pro	Gly
				165					170
Ala	Gly	Gly	Ser	Leu	Ser	Ala	Cys	Ser	Ile
				175					180
Asp	Leu	Pro	Arg	Leu	Ala	Phe	Ala	Pro	Leu

				185					190
Gly	Arg	Lys	Gln	Cys	Ala	Ala	Cys	Leu	Ala
				195					200
Met	His								

<210> 24  
 <211> 239  
 <212> PRT  
 <213> *B. pseudomallei* DD503 bpmR1  
 <400> 24

Met	Glu	Leu	Arg	Trp	Gln	Asp	Ala	Tyr	Leu
1				5					10
Gln	Phe	Ser	Ala	Ala	Glu	Asn	Glu	Gln	Gln
				15					20
Leu	Phe	Gln	Gln	Ile	Ala	Ala	Tyr	Thr	Lys
				25					30
Arg	Leu	Gly	Phe	Glu	Tyr	Cys	Cys	Tyr	Gly
				35					40
Ile	Arg	Val	Pro	Leu	Pro	Ile	Ser	Lys	Pro
				45					50
Val	Val	Ala	Ile	Phe	Asp	Thr	Tyr	Pro	Asn
				55					60
Gly	Trp	Met	Glu	Arg	Tyr	Gln	Glu	Met	Asn
				65					70
Tyr	Leu	Glu	Val	Asp	Pro	Thr	Val	Arg	Glu
				75					80
Gly	Ala	Leu	Ser	Ser	Asn	Met	Ile	Val	Trp
				85					90
Pro	Glu	Ala	Ser	Ala	Ser	Asp	Ala	Thr	Thr
				95					100
Leu	Trp	Ser	Asp	Ala	Arg	Asp	His	Gly	Leu
				105					110
Ala	Val	Gly	Val	Ala	Gln	Ser	Ser	Trp	Ala
				115					120
Ser	Arg	Gly	Val	Phe	Gly	Leu	Leu	Thr	Ile
				125					130
Ala	Arg	His	Thr	Asp	Arg	Leu	Thr	Ser	Ala
				135					140
Glu	Ile	Asn	His	Leu	Thr	Leu	Gln	Ala	Asn
				145					150
Trp	Leu	Ala	Asn	Met	Ser	His	Ser	Leu	Met
				155					160
Ser	Arg	Phe	Leu	Val	Pro	Lys	Leu	Ala	Pro
				165					170
Glu	Ser	Gly	Val	Ala	Leu	Thr	His	Arg	Glu
				175					180
Arg	Glu	Val	Leu	Cys	Trp	Thr	Gly	Glu	Gly
				185					190
Lys	Thr	Ala	Cys	Glu	Ile	Gly	Gln	Ile	Leu
				195					200
Ser	Ile	Ser	Glu	Arg	Thr	Val	Asn	Phe	His
				205					210
Val	Asn	Asn	Ile	Leu	Asp	Lys	Leu	Gly	Ala



215 220  
 Thr Asn Lys Val Gln Ala Val Val Lys Ala  
 225 230  
 Ile Ala Met Gly Leu Ile Asp Ala Pro  
 235

<210> 25  
 <211> 236  
 <212> PRT  
 <213> *B. pseudomallei* DD503 bpmR2  
 <400> 25

Met Glu Met His Asp Phe Leu Gln Phe Trp  
 1 5 10  
 Leu Asn Glu Phe Ser Arg Ser Glu Asn Pro  
 15 20  
 Gln His Val Ile Ser Val Leu Thr Arg Ala  
 25 30  
 Ala Ala Thr Leu Gly Tyr Glu Tyr Ala Ala  
 35 40  
 Tyr Gly Met Arg Arg Pro Phe Pro Ile Ser  
 45 50  
 Asn Pro Pro Ile Leu Met Val Ser Asn Tyr  
 55 60  
 Pro Ala Arg Trp Gln Glu Arg Tyr Ile Glu  
 65 70  
 Ala Arg Phe Ala Asn Ile Asp Gly Ala Val  
 75 80  
 Lys Ala Ala Leu Gly Ser Asp Arg Pro Val  
 85 90  
 Thr Trp Ser Ala Pro Ala Asn Ala Ser Lys  
 95 100  
 Ser Ala Phe Trp Ala Glu Ala Leu Ser Phe  
 105 110  
 Gly Ile Ala His Gly Trp Ser Ser Ala Ser  
 115 120  
 Arg Gly Ala Asp Gly Ala Ile Gly Val Leu  
 125 130  
 Thr Leu Ser Arg Thr Gln Asp Pro Ile Asp  
 135 140  
 Thr Ala Glu Lys Phe Arg Asn Glu Ser Ile  
 145 150  
 Val His Trp Leu Ala Asn Val Ala His Ala  
 155 160  
 Ser Met Ala Pro Phe Leu Pro Ala Ala Asp  
 165 170  
 Glu Phe Asp Pro Asp Leu Thr Arg Arg Glu  
 175 180  
 Thr Asp Val Leu Lys Trp Thr Ala Asp Gly  
 185 190  
 Lys Thr Ala Tyr Glu Ile Ala Leu Ile Leu  
 195 200  
 Ser Ile Ser Glu Ser Thr Val Asn Phe His  
 205 210  
 Val Lys Asn Ile Val Ser Lys Leu Gly Ser

215 220  
 Thr Asn Lys Ile Gln Ala Val Ala Lys Ala  
 225 230  
 Ala Leu Met Gly Met Leu  
 235

<210> 26  
 <211> 230  
 <212> PRT  
 <213> *B. pseudomallei* DD503 bpmR3  
 <400> 26

Met Leu Ser Ala Ala Leu Pro Glu Ser Arg  
 1 5 10  
 Asp Val Arg Thr Leu Val Glu Thr Phe Arg  
 15 20  
 Gln Ala Ala Leu Gln Ile Gly Tyr Gln His  
 25 30  
 His Ala Ile Val Glu Leu Ser Gly Ala Ser  
 35 40  
 His Pro Ala Ser Ile Asp Val Val Ser Leu  
 45 50  
 His Tyr Pro Ser Glu Trp Val Glu His Tyr  
 55 60  
 Thr Arg Asn Asp Tyr Phe Ala Ile Asp Pro  
 65 70  
 Val His Arg Ala Ala Phe Arg Tyr Ser Thr  
 75 80  
 Pro Phe Ser Trp Asn Asp Val Ala Thr Ala  
 85 90  
 Asn Leu Arg Glu Arg His Leu Leu Met Glu  
 95 100  
 Ala Glu Asp Ala Gly Leu Asp Asn Gly Ile  
 105 110  
 Ser Ile Pro Leu His Gln Pro Leu Gly Arg  
 115 120  
 Val Leu Leu Val Ser Leu Ser Gly Thr Ala  
 125 130  
 Pro Thr His Asp Ala Asp Ala Lys Trp Arg  
 135 140  
 Asn Ala Tyr Leu Leu Gly Met Gln Phe Asn  
 145 150  
 Leu Gln Phe Gln Ser Met Arg Thr Cys Arg  
 155 160  
 Pro Ile Pro Pro Ser Val His Leu Thr Asp  
 165 170  
 Arg Glu Gln Met Cys Leu Thr Trp Val Ala  
 175 180  
 Arg Gly Lys Ser Ser Trp Val Ile Ala Asn  
 185 190  
 Met Leu Asp Ile Ser Lys Tyr Thr Val Asp  
 195 200  
 Phe His Ile Glu Asn Ala Met Glu Lys Leu  
 205 210  
 Asn Thr Arg Ser Arg Thr Phe Ala Ala Val

				215					220
Lys	Ala	Thr	Arg	Gln	Glu	Leu	Ile	Phe	Pro
				225					230

&lt;210&gt; 27

&lt;211&gt; 294

&lt;212&gt; PRT

<213> *B. pseudomallei* DD503 bpmR4

&lt;400&gt; 27

Met	Ala	Arg	Thr	Arg	Arg	Gly	Ala	Ser	Glu
1				5					10
Ser	Arg	Arg	Ser	Ala	Arg	Ala	Gly	Ala	Ile
				15					20
Ala	Ala	Arg	Pro	Ala	Phe	Arg	Ala	Arg	Arg
				25					30
Thr	Gly	Gly	Ser	Pro	Arg	Gly	Arg	Ala	Gln
				35					40
Pro	Leu	Ala	Arg	Gly	Gly	Gly	Ala	Arg	Ser
				45					50
Asp	Gln	Pro	Ala	Arg	Arg	Cys	Asp	Asp	Asp
				55					60
Arg	Leu	Arg	Ala	Val	Val	Arg	Ala	Tyr	Leu
				65					70
Ala	Cys	Gly	Val	Arg	Gln	Met	Lys	His	Asp
				75					80
Arg	Ala	Leu	Arg	Asp	Ala	Glu	Asn	Leu	Arg
				85					90
Asp	Phe	Pro	Arg	Arg	Leu	Ala	Ala	Pro	Arg
				95					100
Pro	Leu	Gln	Arg	Phe	Ala	Leu	Ala	Arg	Gly
				105					110
Gln	Ile	Ala	Arg	Ala	Leu	Pro	Ser	Glu	Pro
				115					120
Ala	Ile	Glu	Gln	Leu	Val	His	Arg	Arg	Val
				125					130
His	Glu	Ala	Arg	Glu	Gln	Leu	Arg	Gln	Ala
				135					140
Gln	Gln	Pro	Gln	Tyr	Val	Ala	Arg	Val	Val
				145					150
Leu	Glu	Arg	Ile	Val	Gly	Arg	His	Ala	Glu
				155					160
His	Ala	Asp	Arg	Ala	Ala	Ala	Ile	Val	Asn
				165					170
Gly	Ala	Thr	Glu	Pro	Val	Asp	Glu	Ala	Val
				175					180
Arg	Phe	Arg	Leu	Val	Ala	His	Glu	Leu	Arg
				185					190
Ala	Ala	Gly	Arg	Ile	Glu	Val	Val	Val	Pro
				195					200
Asp	Glu	Arg	His	Gly	Pro	Ala	Pro	Ala	Met
				205					210
Leu	Asn	Asp	Gly	Ile	Asp	Arg	Gln	Val	Val
				215					220
Gly	Gly	Val	Val	Ala	Gln	Pro	Pro	Leu	Gly

	225		230
Arg Lys Ser Val	Glu His Ala Ala Ala	Arg	
	235		240
Arg Arg Ala Gly	Asp Leu Met Pro Val	Arg	
	245		250
Glu Ile Leu Glu	Ala Gln Leu Ala Asn	Val	
	255		260
Ile Arg Arg Leu	Leu Lys Glu Ala Leu	Leu	
	265		270
Asn Ser Arg Val	Gln Asn Phe Val Lys	Arg	
	275		280
Thr Asn Gly Gln	Ala Phe Glu His Arg	Thr	
	285		290
Ala Gln Leu Lys			

&lt;210&gt; 28

&lt;211&gt; 241

&lt;212&gt; PRT

<213> *B. pseudomallei* DD503 bpmR5

&lt;400&gt; 28

Met Arg Ala Ala Met	Gly Asn Trp Ala Glu	
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Asp Leu Leu Ala Gly	Leu Asp Ser Ala Arg	
	15	20
Ser Glu Glu Glu Ala	Phe Arg Ser Val Glu	
	25	30
Thr Ala Ala Ala Ala	Leu Asp Phe Glu Tyr	
	35	40
Cys Ala Tyr Gly Leu	Arg Val Pro Trp Pro	
	45	50
Leu Ser Arg Pro Arg	Ile Glu Thr Arg Ser	
	55	60
Asn Phe Pro Glu Gln	Trp Lys Arg Arg Tyr	
	65	70
Val Glu Ala Gly Phe	Leu Asp Val Asp Pro	
	75	80
Ile Leu Ala His Gly	Arg Arg Ser Gln Gln	
	85	90
Pro Val Val Leu Ala	Glu Thr Leu Phe Ala	
	95	100
Ser Ala His Gln Met	Trp Val Glu Ala Gln	
	105	110
Ser Phe Gly Leu Arg	Phe Gly Trp Ala Gln	
	115	120
Ser Ser Phe Asp Ala	Tyr Gly Gly Met Gly	
	125	130
Met Leu Ala Leu Val	Arg Ser Cys Glu Pro	
	135	140
Val Thr Ala Ala Glu	Leu Asp Ala Lys Glu	
	145	150
Tyr Arg Met Arg Trp	Leu Val Arg Thr Ala	
	155	160
His Ala Ala Leu Gly	Arg Met Met Leu Pro	

	165		170
Lys Leu Met Ala Asp Pro Glu Arg Gly Leu			
	175		180
Thr Glu Arg Glu Val Glu Val Leu Lys Trp			
	185		190
Ala Ala Asp Gly Lys Thr Ser Gly Glu Ile			
	195		200
Ser Lys Ile Leu Ala Ile Ser Val Asp Thr			
	205		210
Val Asn Phe His Val Lys Asn Ala Ile Leu			
	215		220
Lys Leu Arg Thr Ala Asn Lys Thr Ala Ala			
	225		230
Val Val Arg Ala Ala Met Leu Gly Leu Leu			
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Ser			

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